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RAW SEQUENCE LISTING

DATE: 03/19/2002

PATENT APPLICATION: US/10/087,137

TIME: 16:00:18

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J087137.raw

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3 <110> APPLICANT: Deder, Douglas
4   Yamazaki, Victoria
5   Asundi, Vinod
6   Liu, Chenghua
7   Tang, Y. Tom
8   Drmanac, Radoje T.
10 <120> TITLE OF INVENTION: Methods of Therapy and Diagnosis Using Insulin-like Growth
Factor Binding
11   Protein-like Polypeptides and Polynucleotides
13 <130> FILE REFERENCE: HYS-38CIP
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/087,137
16 <141> CURRENT FILING DATE: 2002-02-27
18 <150> PRIOR APPLICATION NUMBER: 09/784,748
19 <151> PRIOR FILING DATE: 2001-02-14
21 <150> PRIOR APPLICATION NUMBER: 09/649,167
22 <151> PRIOR FILING DATE: 2000-08-23
24 <150> PRIOR APPLICATION NUMBER: 09/540,217
25 <151> PRIOR FILING DATE: 2000-03-31
27 <160> NUMBER OF SEQ ID NOS: 14
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 375
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
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41 tcaccggggc gcaggtgggc ctgtcctgtg aagttagggc tgtgcctacc ccagtcatca      180
43 cgtggagaaa ggtcacgaag tcccctgagg gcacccaagc actggaggag ctgcctgggg      240
45 accatgtcaa tatagctgtc caagtgcgag ggggcccttc tgaccatgag gccacggcct      300
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62 atgttctaag tcattttcag tattttacac ccatgttac agatatttga ggtggcttat      180
64 aagacctgta gaaaaaagaa gaaaaatacg taaatggagg aaaccagga aagagcaaaa      240
66 gaagagtagg gacatactta gatgagcagt agaatccctg gtatattctg cacacatctc      300
68 cctctgagct tcttagcatg caaagacaag agctgtgaac atgaagggtgt gtccatgaga      360
70 tgaaaagacc agtttgtgtt tggggctgga gggaatattt cctctgtatt cttttagaaa      420

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85 tcaccggggc gcaggtgggc ctgtcctgtg aagtgaaggc tgtgcctacc ccagtcatca 180
87 cgtggagaaa ggtcacgaag tccccctgagg gcaccaagc actggaggag ctgcctgggg 240
89 accatgtcaa tatagctgtc caagtgcgag ggggcccttc tgaccatgag gccacggcct 300
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106 tgctgcctgt gctgcgcgcg ctgtccccga gccttgggat ccgcgacgtg gcgcgtcggc 180
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112 cgagctgcgg gggcgcgcgc ggcgggcgct gtggcccccg cctgggtatg gcgagccagg 360
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116 gcggtccga cggctcgtcg taccacagcg tctgcgcgct gcgcctgcgc gctcggcaca 480
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126 aacacccat taactttaaa gaaatctcag agggatttgg gaagattttt tcattccagc 780
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130 tgctggatgc cagggtggct gatttgcgtg ccaatgcagc tcctgtggtc gtcgttctc 900
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138 accatgaggc cacggcctgg attttgggtg cagacctgca tcattgtctg aaggtctctc 1140
140 ccacctactc ctactccagc accctttctc cttcacaggt gtttctcta atacatctct 1200
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146 <211> LENGTH: 1009
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148 <213> ORGANISM: Homo sapiens
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (79)..(915)
153 <223> OTHER INFORMATION:
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157 gggcgggag cggtagctgc tcggcgggcg cggagcggag gcgaagcag aggcgcggcc 60

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159	gctgtcccg	agcaagcc	atg	ccg	cgc	ttg	tct	ctg	ctc	ttg	ccg	ctg	ctg	111			
160			Met	Pro	Arg	Leu	Ser	Leu	Leu	Leu	Pro	Leu	Leu				
161			1			5					10						
163	ctt	ctg	ctg	ctg	ctg	ccg	ctg	ctg	ccg	ctg	tcc	ccg	agc	ctc	ggg	159	
164	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Pro	Leu	Ser	Pro	Ser	Leu	Gly		
165			15			20					25						
167	atc	cgc	gac	gtg	ggc	ggc	cgc	ccc	aag	tgt	ggt	ccg	tgc	cgc	cca	207	
168	Ile	Arg	Asp	Val	Gly	Gly	Arg	Arg	Pro	Lys	Cys	Gly	Pro	Cys	Arg	Pro	
169			30			35					40						
171	gag	ggc	tgc	ccg	gcg	cct	gcg	ccc	tgc	ccg	gcg	ccc	ggg	atc	tcg	gcg	255
172	Glu	Gly	Cys	Pro	Ala	Pro	Ala	Pro	Cys	Pro	Ala	Pro	Gly	Ile	Ser	Ala	
173			45			50					55						
175	ctc	gac	gag	tgc	ggc	tgc	tgc	gcc	cgc	tgc	ctg	gga	gcc	gag	ggc	gcg	303
176	Leu	Asp	Glu	Cys	Gly	Cys	Cys	Ala	Arg	Cys	Leu	Gly	Ala	Glu	Gly	Ala	
177	60					65					70						
179	agc	tgc	ggg	ggc	cgc	gcc	ggc	ggg	cgc	tgt	ggc	ccc	ggc	ctg	gta	tgc	351
180	Ser	Cys	Gly	Gly	Arg	Ala	Gly	Gly	Arg	Cys	Gly	Pro	Gly	Leu	Val	Cys	
181						80					85						
183	gcg	agc	cag	gcc	gct	ggg	gca	gcg	ccc	gag	ggc	acc	ggg	ctc	tgc	gtg	399
184	Ala	Ser	Gln	Ala	Ala	Gly	Ala	Ala	Pro	Glu	Gly	Thr	Gly	Leu	Cys	Val	
185						95					100						
187	tgc	gcg	cag	cgc	ggc	acc	gtc	tgc	ggc	tcc	gac	ggt	cgc	tcg	tac	ccc	447
188	Cys	Ala	Gln	Arg	Gly	Thr	Val	Cys	Gly	Ser	Asp	Gly	Arg	Ser	Tyr	Pro	
189						110					115						
191	agc	gtc	tgc	gcg	ctg	cgc	ctg	cgc	gct	cgg	cac	acg	ccc	cgc	gcg	cac	495
192	Ser	Val	Cys	Ala	Leu	Arg	Leu	Arg	Ala	Arg	His	Thr	Pro	Arg	Ala	His	
193						125					130						
195	ccc	ggt	cac	ctg	cac	aag	gcg	cgc	gac	ggc	cct	tgc	gag	ttc	gct	cct	543
196	Pro	Gly	His	Leu	His	Lys	Ala	Arg	Asp	Gly	Pro	Cys	Glu	Phe	Ala	Pro	
197	140					145					150						
199	gtg	gtc	gtc	ggt	cct	ccc	cga	agt	ggt	cac	aac	gtc	acc	ggg	gcg	cag	591
200	Val	Val	Val	Val	Pro	Pro	Arg	Ser	Val	His	Asn	Val	Thr	Gly	Ala	Gln	
201						160					165						
203	gtg	ggc	ctg	tcc	tgt	gaa	gtg	agg	gct	gtg	cct	acc	cca	gtc	atc	acg	639
204	Val	Gly	Leu	Ser	Cys	Glu	Val	Arg	Ala	Val	Pro	Thr	Pro	Val	Ile	Thr	
205						175					180						
207	tgg	aga	aag	gtc	acg	aag	tcc	cct	gag	ggc	acc	caa	gca	ctg	gag	gag	687
208	Trp	Arg	Lys	Val	Thr	Lys	Ser	Pro	Glu	Gly	Thr	Gln	Ala	Leu	Glu	Glu	
209						190					195						
211	ctg	cct	ggg	gac	cat	gtc	aat	ata	gct	gtc	caa	gtg	cga	ggg	ggc	cct	735
212	Leu	Pro	Gly	Asp	His	Val	Asn	Ile	Ala	Val	Gln	Val	Arg	Gly	Gly	Pro	
213						205					210						
215	tct	gac	cat	gag	gcc	acg	gcc	tgg	att	ttg	atc	aac	ccc	ctg	cga	aag	783
216	Ser	Asp	His	Glu	Ala	Thr	Ala	Trp	Ile	Leu	Ile	Asn	Pro	Leu	Arg	Lys	
217	220					225					230						
219	gag	gat	gag	ggt	gtg	tac	cag	tgc	cat	gca	gcc	aac	atg	gtg	gga	gag	831
220	Glu	Asp	Glu	Gly	Val	Tyr	Gln	Cys	His	Ala	Ala	Asn	Met	Val	Gly	Glu	
221						240					245						
223	gct	gag	tcc	cac	agc	aca	gtg	acg	ggt	cta	gat	ctg	agt	aaa	tac	agg	879

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224 Ala Glu Ser His Ser Thr Val Thr Val Leu Asp Leu Ser Lys Tyr Arg
225                               255                               260                               265
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228 Ser Phe His Phe Pro Ala Pro Asp Arg Met
229                               270                               275
231 tacatgttct aagtcatttt cagtatttta cacccatggt atgagatatt tgaggtggct          985
233 tataagacct gtaaaaaaaaa aaaa          1009
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237 <211> LENGTH: 278
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
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248                               20                               25                               30
251 Gly Arg Arg Pro Lys Cys Gly Pro Cys Arg Pro Glu Gly Cys Pro Ala
252                               35                               40                               45
255 Pro Ala Pro Cys Pro Ala Pro Gly Ile Ser Ala Leu Asp Glu Cys Gly
256                               50                               55                               60
259 Cys Cys Ala Arg Cys Leu Gly Ala Glu Gly Ala Ser Cys Gly Gly Arg
260 65                               70                               75                               80
263 Ala Gly Gly Arg Cys Gly Pro Gly Leu Val Cys Ala Ser Gln Ala Ala
264                               85                               90                               95
267 Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val Cys Ala Gln Arg Gly
268                               100                              105                              110
271 Thr Val Cys Gly Ser Asp Gly Arg Ser Tyr Pro Ser Val Cys Ala Leu
272                               115                              120                              125
275 Arg Leu Arg Ala Arg His Thr Pro Arg Ala His Pro Gly His Leu His
276                               130                              135                              140
279 Lys Ala Arg Asp Gly Pro Cys Glu Phe Ala Pro Val Val Val Val Pro
280 145                              150                              155                              160
283 Pro Arg Ser Val His Asn Val Thr Gly Ala Gln Val Gly Leu Ser Cys
284                               165                              170                              175
287 Glu Val Arg Ala Val Pro Thr Pro Val Ile Thr Trp Arg Lys Val Thr
288                               180                              185                              190
291 Lys Ser Pro Glu Gly Thr Gln Ala Leu Glu Glu Leu Pro Gly Asp His
292                               195                              200                              205
295 Val Asn Ile Ala Val Gln Val Arg Gly Gly Pro Ser Asp His Glu Ala
296                               210                              215                              220
299 Thr Ala Trp Ile Leu Ile Asn Pro Leu Arg Lys Glu Asp Glu Gly Val
300 225                              230                              235                              240
303 Tyr Gln Cys His Ala Ala Asn Met Val Gly Glu Ala Glu Ser His Ser
304                               245                              250                              255
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308                               260                              265                              270
311 Ala Pro Asp Asp Arg Met
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315 <210> SEQ ID NO: 7

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325 tgccggccag agggctgccc ggcgcctgcg ccctgcccgg cgcccgggat ctcggcgctc      180
327 gacgagtgcg gctgctgcgc ccgctgcctg ggagccgagg gcgcgagctg cgggggccgc      240
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331 gagggcaccg ggctctgcgt gtgcgcgcag cgcggcaccg tctgcggctc cgacggtcgc      360
333 tegtacccca gcgtctgcgc gctgcgcctg cgcgctcggc acacgccccg cgcgcacccc      420
335 ggtcacctgc acaaggcgcg cgacggccct tgcgagttcg ctctgtggt cgtcgttctt      480
337 ccccgaaagtg ttcacaacgt caccggggcg caggtgggccc tgtcctgtga agtgagggct      540
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341 ctggaggagc tgccctgggga ccatgtcaat atagctgtcc aagtgcgagg gggcccttct      660
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345 taccagtgcc atgcagccaa catggtggga gaggtgagt cccacagcac agtgacggtt      780
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352 <212> TYPE: PRT
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355 <400> SEQUENCE: 8
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366 <400> SEQUENCE: 9
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373          20          25
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377 <211> LENGTH: 251
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392          35          40          45
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396          50          55          60
399 Ala Ser Gln Ala Ala Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val
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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
